

First molecular characterization of *Giardia duodenalis* from goats in Malaysia

ABSTRACT

In the present study, 310 faecal samples from goats from eight different farms in Malaysia were tested for the presence of *Giardia* using a PCR-coupled approach. The nested PCR for SSU amplified products of the expected size (~200 bp) from 21 of 310 (6.8%) samples. Sixteen of these 21 products could be sequenced successfully and represented six distinct sequence types. Phylogenetic analysis of the SSU sequence data using Bayesian Inference (BI) identified *Giardia* assemblages A, B and E. The identification of the 'zoonotic' assemblages A and B suggests that *Giardia*-infected goats represent a possible reservoir for human giardiasis in Malaysia.

Keyword: *Giardia duodenalis*; Small subunit of the nuclear ribosomal RNA (SSU) gene; Goats; Malaysia.